```
================================================================
Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Thu May 03 16:48:36 EDT 2007
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*************************************************************
Reviewer Comments:
<210>    4
<211>    6223
<212>    DNA
<213>    crt gene

<400>    4
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The <213> response is invalid. Per 1.823 of Sequence Rules, the only
valid <213> responses are: "Artificial Sequence," "Unknown," or the
Genus/species. FYI: if this is an Artificial Sequence, then "crt gene"
would be an insufficient explanation (please explain the source of the
genetic material in the <223> response).

Same type of error in sequences 5-16
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Validated By CRFValidator v 1.0.2

Application No: 10551508   Version No: 1.0

Input Set:

Output Set:

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           Finished:  2007-05-03 16:08:58.290
            Elapsed:  0 hr(s) 0 min(s) 0 sec(s) 384 ms
     Total Warnings:  4
       Total Errors:  0
No. of SeqIDs Defined:  18
  Actual SeqID Count:  18
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ErrCode	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

<110>   KIM, Young Tae
         LEE, Jae Hyung

<120>   Gene involved in the biosynthesis of carotenoid and marine
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<130>   428.1056

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Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
        35   40   45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Phe Ile Ala
    50   55   60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Gly Asn
 65   70   75   80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
                85   90   95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Thr Gly Thr
            100   105   110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
            115   120   125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
    130   135   140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145   150   155   160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
            180   185   190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
        195   200   205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys
        35   40   45

Asn Asp Leu Tyr Gly Leu Val Phe Ala Val Ile Ala Thr Val Leu Phe
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Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly
 65   70   75   80

Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val
            85   90   95

His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg
            100   105   110

Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
        115   120   125

His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
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Lys Gln Asp Leu Lys Thr Ser Gly Val Leu Arg Ala Glu Ala Gln Glu
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Arg Thr

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Leu Asp His Ala Ala Gly Pro Ser Asp Gly His Thr Trp Ser Cys His
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